

OM of: us-09-743-492-1 to: PIR_68:* out_format : pfs

Date: May 13, 2002 9:45 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters: -DB=us-09-743-492-1

-MODEL=frame-n2p.model -DRV=xlp
-Q/cgml2/USPTO_spool/US09743492/runat_13052002_093834_19627/app_query.fasta_1.3580
-DB=PIR_68 -QMT=fastan -SUFFIX=tr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-ALIGN=50 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-LIST=20 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09743492 -CGN1_1_269 -NCPU=6 -ICPU=3
-LOGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-743-492-1

Query length: 3467

Database: PIR_68*

Database sequences: 219241

Database length: 76174552

Search time (sec): 161.560000

score_list:

Seq	Strd	Orig	ZScore	Escore	Len	Documentation
pir1.TDHULK	+ 3236.00	3838.56	4.2e-207	1897	1	leukocyte antigen-related protein
pir1.A56493	+ 3176.50	3771.13	3.6e-203	1290	1	leukocyte common antigen-related protein
pir2.S46216	+ 3172.00	3762.20	7.6e-203	1898	1	leukocyte antigen-related protein
pir2.A57068	+ 3057.00	3635.89	2.7e-195	582	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.D546178	+ 2926.00	3468.63	1.7e-186	1912	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.D546178	+ 2874.50	3408.32	4.4e-183	1691	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.C54689	+ 2874.50	3407.27	4.5e-183	1894	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.I50212	+ 2867.50	3401.08	1.3e-182	1499	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.I58148	+ 2850.00	3380.18	1.8e-181	1501	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.S50893	+ 2847.00	3374.40	3.0e-181	1907	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.S46217	+ 2844.00	3371.03	4.8e-181	1863	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A48758	+ 2753.50	3265.08	4.7e-175	1496	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.S53089	+ 2509.00	2975.17	8.1e-159	1231	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.TDFELK	+ 2503.00	2963.40	2.2e-158	2029	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.T31093	+ 2450.50	2903.95	6.4e-155	1437	1	probable protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.I56540	+ 1869.00	2222.00	2.2e-116	398	1	receptor tyrosine phosphatase (EC 2.7.1.1)
pir1.T19121	+ 1836.50	2170.48	4.2e-114	1585	1	probable protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.A36065	+ 1551.00	1836.14	3.4e-95	802	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.B48758	+ 1538.00	1816.45	2.7e-94	1262	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.JC1285	+ 1525.00	1805.19	1.8e-93	796	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A47373	+ 1518.00	1796.46	5.4e-93	829	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.S12053	+ 1429.00	1691.83	4.3e-87	700	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.JC6132	+ 1423.00	1684.69	1.1e-86	699	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.S17670	+ 1307.00	1539.55	6.3e-79	1452	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.S17669	+ 1306.00	1538.36	7.3e-79	1452	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A48066	+ 1243.00	1463.16	1.1e-74	1440	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.JC6312	+ 1236.00	1454.92	3.3e-74	1440	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A48148	+ 1168.00	1373.75	1.1e-69	1445	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.JC5290	+ 1166.50	1372.02	1.4e-69	1436	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.B48148	+ 1162.00	1366.61	2.7e-69	1442	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.T42636	+ 1142.00	1342.88	5.8e-68	1422	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.S72441	+ 1135.50	1335.00	1.6e-67	1442	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A46151	+ 1117.50	1309.16	2.7e-66	2314	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.A41622	+ 1089.50	1281.06	1.8e-64	1301	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.A54080	+ 1048.50	1232.61	9.2e-62	1237	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.TDFELT	+ 1038.00	1219.82	4.6e-61	1273	1	leukocyte common antigen precursor
pir1.A46546	+ 1035.50	1216.62	6.8e-61	1304	1	leukocyte common antigen long
pir1.A28334	+ 1017.00	1194.64	1.2e-59	1291	1	protein-tyrosine-phosphatase (EC 2.7.1.1)
pir2.T43148	+ 1013.00	1190.54	2.1e-59	1200	1	probable protein-tyrosine-phosphatase (EC 2.7.1.1)
pir1.B36182	+ 1011.50	1186.93	2.7e-59	1462	1	protein-tyrosine-phosphatase (EC 2.7.1.1)

pir2.T42522	+ 894.00	1047.08	1.8e-51	1409	1	protein-tyrosine-phosphatase
pir2.T30111	+ 876.50	1026.12	2.6e-50	1422	1	hypothetical protein F56D1.1
pir1.A55148	+ 702.00	816.21	1.0e-38	1711	1	protein-tyrosine-phosphatase
pir2.A40169	+ 697.00	827.77	1.6e-38	256	1	protein-tyrosine-phosphatase
pir2.T23738	+ 635.00	744.37	2.5e-34	711	1	hypothetical protein T13H5.1
pir2.T23308	+ 634.50	739.30	3.0e-34	1156	1	hypothetical protein K04D7.1
pir2.T14328	+ 631.00	728.77	5.8e-34	2302	1	protein-tyrosine-phosphatase
pir1.A49724	+ 625.00	728.27	1.3e-33	1118	1	protein-tyrosine-phosphatase
pir2.A49502	+ 611.50	707.94	1.1e-32	1767	1	protein-tyrosine-phosphatase

seq_name: pir1.TDHULK

seq_documentation_block:

leukocyte antigen-related protein precursor - human

N:Alternate names: leukocyte common antigen homolog

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999

C:Accession: S03841; J10051

R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.

J. Exp. Med. 168, 1523-1530, 1988

A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region

A:Reference number: J10051; MUID:89035978

A:Accession: S03841

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1897 <STR>

A:Cross-references: EMBL:Y00815; NID:934266; PIDN:CAA68754.1; PID:934267

C:Genetics:

A:Gene: GDB:PTPRF; LAR

A:Cross-references: GDB:L20138; OMIM:179590

A:Map position: lp34-lp34

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>

F:17-1250/Domain: extracellular #status predicted <EXT>

F:37-99/Domain: immunoglobulin homolog <IMM1>

F:139-199/Domain: immunoglobulin homolog <IMM2>

F:236-290/Domain: immunoglobulin homolog <IMM3>

F:308-390/Domain: fibronectin type III repeat homolog <FN3A>

F:403-489/Domain: fibronectin type III repeat homolog <FN3B>

F:501-583/Domain: fibronectin type III repeat homolog <FN3C>

F:596-685/Domain: fibronectin type III repeat homolog <FN3D>

F:698-798/Domain: fibronectin type III repeat homolog <FN3E>

F:810-893/Domain: fibronectin type III repeat homolog <FN3F>

F:905-989/Domain: fibronectin type III repeat homolog <FN3G>

F:1001-1078/Domain: fibronectin type III repeat homolog <FN3H>

F:1251-1274/Domain: transmembrane #status predicted <TM>

F:1275-1897/Domain: intracellular #status predicted <INT>

F:1285-1897/Domain: leukocyte common antigen cytosolic domain homolog <LAC>

F:1365-1586/Domain: protein-tyrosine-phosphatase homolog <PTP1>

F:1654-1877/Domain: protein-tyrosine-phosphatase homolog <PTP2>

F:44-97, 146-197, 243-288/Disulfide bonds: #status predicted

F:107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1544/Binding site: substrate phosphate (Arg) #status predicted

F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1835/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality:	3236.00	Length:	607
Ratio:	5.331	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-743-492-1 x TDHULK

Align seg 1/1 to: TDHULK from: 1 to: 1897

6 GGACTGAAGGACTCCTTGCTGGCCCACTCCTCTGACCCCTGTGGAGATGCG 55

1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetAr 1307
56 GAGCTCAACTACAGACCCAGAGTATGCGAGACCCAGCCACCATCCCA 105
1307 GArGLeuAsnTyRGlnThrProGlyMetArgAspHisProProlleProI 1324
106 TCACCGACCTGGGGCAACACATCGAGCGCTCAAGCCAAACGATGGCTC 155
1324 leThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeu 1340
156 AAGTTCTCCAGAGATGATGATCCATCGACCCCTGGAGCAGATTCAGGTG 205
1341 LysPheSerGlnGlnTyRGluSerIleAspProGlyGlnGlnPheThrTr 1357
206 GGAGAAATCAACCTGGAGTGAACAGCCCAAGACCCGCTATCCGAATG 255
1357 pGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyRAlaAsnV 1374
256 TCATCGCCTACGACCACTCTCGAGTCACTCTTACCTCTATCGATGGCTC 305
1374 alIleAlaTyRAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
306 CCGGGAGTCACTACATCAATGCCAATGATCATGATGGCTACCGCAAGCA 355
1391 ProGlySerAspTyRileAsnAlaAsnTyRileAspGlyTyRArgLysGI 1407
356 GAATGCTTACATGCCACGACGAGCGCCCTGCGCCGAGACCATGGCGATT 405
1407 nAsnAlaTyRileAlaThrGlnGlyProLeuProGluThrMetGlyAspP 1424
406 TCTGGAGAAATGGTGGGAACAGCGCACGCGCCACTGTGTTCATGATGACA 455
1424 heTrpArgMetValTrpGluGluArgThrAlaThrValValMetMetThr 1440
456 CGGCTGGAGAGAGTCCCGGGTAAATGTGATCAGTACTTGGCCAGCCCG 505
1441 ArgLeuGluGlnLysSerArgValLysCysAspGlnTyRtrpProAlaAr 1457
506 TGGCACCAGACCTGTGGCTTATTACAGTGCACCTGTGGACACAGTGG 555
1457 gGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValG 1474
556 AGCTGGCCACATACATGTGCGCACCTTCGCATCCACAGAGTGGCTCC 605
1474 luLeuAlaThrTyRThrValArgThrPheAlaLeuHisLysSerGlySer 1490
606 AGTGAGAGCGTCAGCTGGCTCAGTTTCAGTTTCATGCGCTGGCCAGACCA 655
1491 SerGlyLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHI 1507
656 TGGAGTTCCTGAGTACCCAACTCCCATCCTGGCTTCCTACGACGGGTCA 705
1507 sGlyValProGluTyRProThrProIleLeuAlaPheLeuArgArgValL 1524
706 AGCCCTGCACACCCCTAGACGAGGCCCATGTGTGTGCTACTCCAGCGGG 755
1524 ysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAla 1540
756 GCGGTGGCGCCAGCGCTGCTTCATCGTATTGATGCCATGTGGAGCG 805
1541 GlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluAr 1557
806 GATGAAGCAGCAGAGACGGTGACATCTATGGCCACGCTGACCTGCATGC 855
1557 gMetLysHisGluLysThrValAspIleTyRGlyHisValThrCysMeta 1574
856 GATCAGAGGAACTACATGGTGCAGACGAGGAGCAGTACGTGTTTCATC 905
1574 rgSerGlnArgAsnTyRMetValGlnThrGluAspGlnTyRValPheIle 1590
906 CATGAGGCGCTGCTGGAGGCTGCCAGTGGCGCCACACAGAGTGGCTGC 955

1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAl 1607
956 CCCAACCTCTATGCCACATCCAGAGCTGGCCAAAGTCCCTCCAGGGG 1005
1607 aArgAsnLeutyRAlaHisIleGlnLysLeuGlyGlnValProProGlyG 1624
1006 AGAGTGTGACCGCATCGAGTTCAGTTCAAGTTGCTGGCCAGCTCCAAG 1055
1624 luSerValThrAlaMetGluLeuGluPheLysLeuLeuAlaSerSerLys 1640
1056 GCCCAGACGTCCTTCATCATCAGCGCAACCTGCCCTGCAACAGTTCAA 1105
1641 AlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLy 1657
1106 GAACCGCTGGTGAACATCATGCCCTACGAATTCACCCGTGTGTCTGTC 1155
1657 sAsnArgLeuValAsnIleMetProTyRGluLeuThrArgValCysLeuG 1674
1156 AGCCCATCCGTGTGTGGAGGCTCTGACTACATCATATGCAGCTTCCTG 1205
1674 lnProIleArgGlyValGluGlySerAspTyRileAsnAlaSerPheLeu 1690
1206 GATGCTTATAGACAGCAGAGGCTTACATAGCTACAGAGGGCTCTGGC 1255
1691 AspGlyTyRArgGlnGlnLysAlaTyRileAlaThrGlnGlyProLeuAl 1707
1256 AGAGACACCGAGGACTTCTGGCGCATGCTATGGAGCACAATTCACACCA 1305
1707 aGluSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSerThrI 1724
1306 TCATCGTCAATGTGACCAAGCTTCGGGAGATGGGAGGAGAAATGCCAC 1355
1724 leIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHis 1740
1356 CACTACTGGCCACAGAGCGCTCTGCTCGCTACAGTACTTCTGTTTGA 1405
1741 GlnTyRtrpProAlaGluArgSerAlaArgTyRGlnTyRtrpPheValValAs 1757
1406 CCGATGGTGTGATACAACATGCCAGTATATCCTCGCTGAGTTCAAGG 1455
1757 pProMetAlaGluTyRAsnMetProGlnTyRileLeuArgGluPheLysV 1774
1456 TCACGGATGCCGGGATGGGCAGTCAAGGACAATCCGGCAGTTCAGTTCC 1505
1774 alThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGACTGGCCAGACGAGCGGTGCCCAAGACAGCGGAGGATTCATTGA 1555
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAs 1807
1556 CTTTCATCGGGCAGGTGCATAAGACCAAGACAGTTCGGACAGATGGGC 1605
1807 pPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAspGlyP 1824
1606 CTATCAGGTGCTACTGCTGCTGGCGTGGCGCCGCGCCGGGTGTTTCATC 1655
1824 roIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIle 1840
1656 ACPTCTGAGCATGCTCTGGAGCGCATGCGTATGAGGCGTGTGTCACAT 1705
1841 ThrLeuSerIleValLeuGluArgMetArgTyRGlyGlyValValAspMe 1857
1706 GTTTCAGACCGTGAAGACCTCGTACACAGCGTCTCTGCCATGGTGACAGA 1755
1857 tPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnI 1874
1756 CAGAGACCGATATCAGTGTGCTACCGTGGCGCCCTCGAGTACCTGGCC 1805
1874 hrGluAspGlnTyRGlnLeuCysTyRArgAlaAlaLeuGluTyRLeuGly 1890
1806 AGCTTTGACCACTATCAACG 1826
1891 SerPheAspHisTyRAlaThr 1897

seq_name: pir2:A56493

seq_documentation_block:

Leucocyte common antigen-related protein (LAR) - rat (fragment)

N:Alternate names: LAR receptor-linked tyrosine phosphatase

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: A56493; 155393

R:Zhang, J.S.; Longo, F.M.

J. Cell Biol. 128, 415-431, 1995

A:Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the

A:Reference number: A56493; MUID:95146548

A:Accession: A56493

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1290 <RES>

A:Cross-references: EMBL:X83505; NID:q732918; PIDN:CAA58495.1; PID:q732919

P:Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.

Biol. Chem. 268, 26503-26511, 1993

Abstract: Leucocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation

A:Reference number: 155393; MUID:94075340

A:Accession: 155393

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 831-1290 <RE2>

A:Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:80-166/Domain: fibronectin type III repeat homology <3FP>

F:667-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1047-1270/Domain: protein-tyrosine-phosphatase homology <PIP2>

F:931/Active site: Cys (phosphocysteine intermediate) #status predicted

F:937/Binding site: substrate phosphate (Arg) #status predicted

F:1222/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1228/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 3176.50 Length: 618

Ratio: 5.268 Gaps: 1

Percent Similarity: 97.573 Percent Identity: 96.926

alignment_block:

US-09-743-492-1 x A56493

align seg 1/1 to: A56493 from: 1 to: 1290

6 GCAGTCAAGGACTCTGCTGCGCCACTCTCTGACCCCTGTGGAGATGCG 55

673 GlyLeuLysAspSerLeuLeuAlaHisSerAspProValGluMetAr 689

56 GAGGCTCAACTACACACCCAGGT..... 80

689 gArgLeuAsnTyrGlnThrProGlySerSerAlaProSerCysProAsnI 706

81ATCGGAGACCAACCCATCCCATCCAGCCTGGCGGAC 122

706 leSerSerMetArgAspHisProProIleProIleThrAspLeuAlaAsp 722

123 ACATCGAGCGCCTCAAGCCCAACGATGCGCTCAAGTCTCCAGAGTA 172

723 AsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyr 739

173 TCAGTCCATCGACCTGGACACAGTTCACGTGGGAGATTCAAACTGG 222

739 rGluSerIleAspProGlyGlnGlnPheThrIrpGluAsnSerAsnSerg 756

223 AGGTGAACCAAGCCCAAGAACCGCTATCGGAATGCTATCGCTTACGACCA 272

756 luValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHis 772

273 TCTCGAGTCACTCTTACCTCTATCTGATGCGGTCCTCCCGGGAGTCACTACAT 322

773 SerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyrIle 789

323 CAATGCCAACTACATCGATGGCTACCGCAAGCAGAGATGCTTACATCGCCA 372

789 eAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaT 806

373 CGCAGGGCCCTGCGCCAGACCATGGCGATTCTGGAGAAATGGTGTGG 422

806 hrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrp 822

423 GAACAGCGACGCGCACTGTGTCATGATGACACGCGCTGGAGGAGAATC 472

823 GluGlnArgThrAlaThrValMetMetThrArgLeuGlnGlnLys 839

473 CGGGTAAATGTGATCAGTACTGGCCAGCCGCTGGCACCAGAGACCTGTG 522

839 rArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrTyrG 856

523 GCCTTATTCAGGTGACCCCTGTGGACACAGTGGAGCTGGCCACATACACT 572

856 lylLeuIleGlnValThrLeuValAspThrValGluLeuAlaThrTyrThr 872

573 GTGCGCACCTTCGCACCTCCACAGAGTGGCTCCAGTGAGAAGCGTGAGCT 622

873 MetArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGluLe 889

623 GGCTCAGTTTTCAGTTTCATGCGCTGGCCAGACCATGGAGTTCCTGAGTACC 672

889 uArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrP 906

673 CAACTCCCATCTCGGCTCTTACAGACGGGTCAAGCCCTGCAACCCCTTA 722

906 roThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeu 922

723 GACGACGAGCCCATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772

923 AspAlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGl 939

773 CTGCTTCATCGTATGATGATGATGATGATGATGATGATGATGATGATGAT 822

939 yCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 956

823 CGGTGGACATCTATGCCACGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 872

956 hrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyr 972

873 ATGGTGCACAGGAGGACGACGATGATGATGATGATGATGATGATGATGATG 922

973 MetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuGl 989

923 GGCTGCGCAGCTGCGGCCACACAGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 972

989 uAlaAlaMetCysGlyHisThrGluValLeuAlaArgAsnLeuTyrAlaH 1006

973 ACATCCAGAGCTGGGCCCAAGTGCCTCCAGGGGAGAGTGTGACCCCATG 1022

1006 lsIleGlnLysLeuGlyGlnValProProGlyValSerValThrAlaMet 1022

1023 GAGCTCGAGTTCAAGTTGCTGGCCAGCTCAAGGCCACACGCTCCCGCTT 1072

1023 GluLeuGluPheLysLeuLeuAlaAsnSerLysAlaHisThrSerArgPh 1039

1073 CATCAGCGCAACCTGCGCTGCAACAAGTTCAGAAACCCGCTGGTGAACA 1122

1039 eIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnI 1056

1123 TCATGCCCTTACGAATGACCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1172

1056 leMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyVal 1072

1173 GAGGGCTGCTGACTACATCAATGCCAGCTTCTGCTGATGGTTATAGACAGCA 1222
 |||||
 1073 GluclySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnG1 1089
 |||||
 1223 GAGGGCTGCTGACTACATCAATGCCAGGGGCTCTGGCAGAGACCGAGACT 1272
 |||||
 1089 nLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAsp 1106
 |||||
 1273 TCTGGCGCATGCTATGGGAGCAAAATCCACCATCATCGTCGCTGACC 1322
 |||||
 1106 heTrpargMetLeuTrpGluHisAsnSerThrIleValMetLeuThr 1122
 |||||
 1323 AAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCAGCAGA 1372
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 1123 LysLeuArgGluMetGlyArgGluGlyCysHisGlnTyrTrpProAlaG1 1139
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 1373 GCCTCTGCTGCTACAGTACATCTTCTGTTGACCCGATGGCTGAGTACA 1422
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 1139 uArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrA 1156
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 1423 ACATGCCCATGATATCTCTGCTGAGTTCAGGCTCAGGATGCCGGGAT 1472
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 1156 snMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArgAsp 1172
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 1473 GGGCAGTCAAGGACAAATCCGGCAGTTCAGTTCACAGTCCGACGAGCA 1522
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 1173 GlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGluG1 1189
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 1523 GGGCGTGGCCCAACAGCGGAGGATTCATTGACTTCATCGGCGCAGTGC 1572
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 1189 nGlyValProLysThrGlyGluGlyPheIleAspPheIleGlyGlnValH 1206
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 1223 SerAlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValle 1239
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 1289 aThr 1290

seq_name: p1r2.S46216

seq_documentation_block:

leukocyte antigen-related protein precursor - rat

N:Alternate names: leukocyte common antigen homolog

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S46216; S23252; A41032; A33154

B:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 59-47, 1994

A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph

A:Reference number: S46216; MUID:94347119

A:Accession: S46216

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1898 <ZHA>

A:Cross-references: EMBL:U11586; NID:g205132; PIDN:AAC37655.1; PID:g205133
 R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
 Biochem. J. 284, 569-576, 1992
 A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by t
 A:Reference number: S23126; MUID:92287069
 A:Accession: S23252
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1361-1604; 1649-1898 <HAS>
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 J. Biol. Chem. 266, 19688-19696, 1991
 A:Title: Cloning, bacterial expression, purification, and characterization of the cyt
 A:Reference number: A41032; MUID:92011772
 A:Accession: A41032
 A:Molecule type: mRNA
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
 A:Cross-references: GB:M60103; NID:g205130; PIDN:AAA41510.1; PID:g205131
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 submitted to the Protein Sequence Database, December 1990
 A:Reference number: A33154
 A:Accession: A33154
 A:Molecule type: mRNA
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
 C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphat
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
 ogy

C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase
 F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
 F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <
 F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
 F:47-109/Domain: immunoglobulin homology <IMM1>
 F:149-209/Domain: immunoglobulin homology <IMM2>
 F:246-300/Domain: immunoglobulin homology <IMM3>
 F:318-400/Domain: fibronectin type III repeat homology <FN3A>
 F:413-439/Domain: fibronectin type III repeat homology <FN3B>
 F:511-533/Domain: fibronectin type III repeat homology <FN3C>
 F:608-635/Domain: fibronectin type III repeat homology <FN3D>
 F:708-739/Domain: fibronectin type III repeat homology <FN3E>
 F:811-835/Domain: fibronectin type III repeat homology <FN3F>
 F:906-930/Domain: fibronectin type III repeat homology <FN3G>
 F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>
 F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>
 F:1276-1898/Domain: intracellular #status predicted <INT>
 F:1386-1587/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1555-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F:54-107, 156-207, 253-298/Disulfide bonds: #status predicted

F:117, 250, 295, 721, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1545/Binding site: substrate phosphate (Arg) #status predicted
 F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1836/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 3172.00 Length: 607

Ratio: 5.269 Gaps: 0

Percent Similarity: 99.176 Percent Identity: 98.188

alignment_block:

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1292 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetAr 1308

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56 GAGGCTCAACTACACACCCAGGATGCGAGACCAACCCACCATCCCA 105

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1308 gArgLeuAsnTyrGlnThrProGlyMetArgAspHisProProIleProI 1325

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106 TCACCGACCTGGCGGACAAACATCGAGCGCTCAACAGCCACGATGCCCTC 155

1325 leThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeu 1341
1356 AAGTCTCCAGGAGATGATGCTCATCGACCTGGACAGCAGTTCACGGT 205
1342 LysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTr 1358
206 GGAGAAATTCAAACCTGGAGGTCAACAAGCCCAAGACCGCTATGCGAATG 255
1358 pGluAsnSerAsnSerGluValAsnLysProLysAsnArgTyrAlaAsnV 1375
256 TCATCGCCTACGACCACTCTCGAGTCATCTTACCTCTATCGATGCGCTC 305
1375 alileAlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyVal 1391
306 CCGGGAGTACTACATCAATGCCAACTACATCGATGGCTACCGCAAGCA 355
1392 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysG 1408
356 GAATGCCTACATCGCACGACGGGCCCTCGCCGAGACCATGGCGGATT 405
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406 TCTGGAATGTGTGGGAACAGCCAGCCGCTGTGGTCTATGATGACA 455
1425 heTrpArgMetValTrpGluGlnArgIleAlaThrValValMetMetThr 1441
456 CGGCTGGAGGAGAAGTCCCGGTAATGTGATCATGACTGCTGCCAGCCGG 505
1442 ArgLeuGluGluLysSerArgValLysCysAspGlnTyrTrpProAla 1458
506 TGGCACCGAGACCTGTGGCTTATTTCAGGTGACCTGTGGACACAGTGG 555
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556 AGCTGGCCCATACACTGTGGCCACTTCGCACCTCCACAAAGAGTGGCTCC 605
1475 luLeuAlaThrTyrThrMetArgThrPheAlaLeuHisLysSerGlySer 1491
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1492 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHi 1508
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906 CATGAGGCGCTGCTGAGGCTGCCAGCTGGCGGCCACACAGAGGTGCTGCG 955
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1608 aArgAsnLeuTyrAlaHisIleGlnLysLeuGlyGlnValProGlyG 1625
1006 AGAGTGTGACCCGCTAGAGCTGAGCTGAGTCAAGTGTGCGCCAGCTCCAA 1055

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1642 AlaArgAlaSerArgPheIleSerAlaAsnLeuProCysAsnLysPhe 1658
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1658 sasnArgLeuValAsnIleMetProTyrGluLeuThrArgValCysLeu 1675
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1875 hrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1891
1806 AGCTTTGACCACTATGCAACG 1826
1892 SerPheAspHisTyrAlaThr 1898

seq_name: pir2:A57068

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
N;Alternate names: leukocyte antigen-related protein LAR
C;Species: Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999

C:Accession: A57068; S40280
R:Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
Genomics 27, 124-130, 1995
A:Title: The mouse gene ptpfr encoding the leukocyte common antigen-related molecule LAR
A:Reference number: A57068; MUID:95394448
A:Accession: A57068
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-582 <SB>
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R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases
A:Reference number: S40280
A:Accession: S40280
A:Molecule type: mRNA
A:Residues: 116-221 <HEN>
A:Cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136
C:Genetics:
A:Gene: Ptpfr
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
og
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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F:50-271/Domain: protein-tyrosine-phosphatase homology <PTP1>
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Quality: 3057.00 Length: 582
Ratio: 5.289 Gaps: 0
Percent Similarity: 99.313 Percent Identity: 98.282

alignment_block:

US-09-743-492-1 x A57068 ..

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131 GCGCCTCAAAGCCAAAGCATGGCTCAAGTTCTCCAGGAGTATGAGTCCA 180
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17 uArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerI 34
181 TCGACCTGGACAGCAGTTCACGTGGGAGAAATTCAAACCTGGAGGTGAAC 230
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34 LeAspProGlyGlnGlnPheThrTrpGluAsnSerAsnSerGluValAsn 50
231 AAGCCCAAGAACCGCTATGGGATGTCATCGCTACGACCACTCTCGAGT 280
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51 LysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVa 67
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67 lLeuLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaA 84
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381 CCCCTGCCGAGACCATGGCGGATTTCTGGAGAAATGGTGTGGGAACAGCG 430
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431 CACGGCCACTGTGTATGATGATACCGCTGGAGGAGAGTCCCGGGTAA 480
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117 gThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgVal 134

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134 yscysaspGlnTyrTrpProValArgGlyThrGluThrTyrGlyLeuIle 150
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151 GlnValThrLeuValAspThrValGluLeuAlaThrTyrThrMetArgTh 167
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201 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaG1 217
731 GCCATGGTGGTGCACGTGACGCGCGGCTGGCCGCGCCGCGCTGCTTCA 780
217 yProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheI 234
781 TCCTGATTGATGCATGCTTGGAGCGGATGAAGCAGCAGAGAGACGGTGGAC 830
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seq_documentation_block:
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N:Alternate names: WPTP delta type D
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: D54689; A54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: WPTP delta, a putative murine homolog of HPTP delta, is expressed in special
A:Reference number: A54689; MUID:93360986
A:Accession: D54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1691 <M12>
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:P136537)
A:Accession: A54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398,799-1691 <M12>
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBI:P136524)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
ogy
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
F;42-95/Domain: immunoglobulin homology <IMM3>
F;114-196/Domain: fibronectin type III repeat homology <FN3A>
F;1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1449-1671/Domain: protein-tyrosine-phosphatase homology <ptp2>
F;1333/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1339/Binding site: substrate phosphate (Arg) #status predicted
F;1623/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1629/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:
Quality: 2874.50 Length: 599
Ratio: 4.956 Gaps: 3
Percent Similarity: 96.828 Percent identity: 89.149

alignment_block:

US-09-743-492-1 x D54689

Align seg 1/1 to: D54689 from: 1 to: 1691

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1096 HisProThrAspProValGluLeuArgLeuAsnPheGlnThrProG 1112
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
80  TATCGAGACCCACCACCCATCCCATCCAGCTGCGCGGACAAACATCG 129
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1112 yMetAlaSerHisProProIleLeuGluLeuAlaAspHisIleG 1129
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
130  AGCGCTCAAGCAACGATGCGCTCAAGTTCTCCAGGAGTATGAGTCC 179
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1129 luArgLeuLysAlaAsnAspAsnLeuLysPheSerGlnGluTyrGlu 1145
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
180  ATCGACCTGGGACAGATTACGTGGGAGAATTCAACCTGGAGGTGAA 229
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1146 IleAspProGlyGlnGlnPheThrTrpGluHisSerAsnLeuGluVal 1162
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
230  CAAGCCCAAGACCGCTATGCGAATGTCATCGCTACGACCTCTCGAG 279
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1162 nLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArg 1179
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
280  TCATCCTTACCTCTATCGATGGCTCCCGCGGAGTGACTACATCATG 329
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1179 aluLeuSerAlaIleGluGlyIleProGlySerAspTyrValAsnAla 1195
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
330  AACTACATCATGGGTACCGCAGCAGAAATGCTACATCCCGCAGCAGG 379
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1196 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGln 1212
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
380  CCCCCTGCCGAGACCATGGCGATTTCTGGAGATGGTGGGAAACAGC 429
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1212 ySerLeuProGluThrPheGlyAspPheTrpArgMetIleTrpGluGln 1229
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
430  GCAGCGCCACTGTGTCATGATGACACCGCTGGAGGAGAGTCCCGGTA 479
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1229 lu...AlaThrValMetMetMetMetMetMetMetMetMetMetMet 1244
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
480  AATGTGATGACTGCTGCGCAGCCGCTGGCAGCAGACCTGTGGCTTAT 529
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1245 LysCysAspGlnTyrTrpProSerArgGlyThrGluThrHisGlyLeu 1261
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
530  TCAGTGACCCCTGTGGACACAGTGGAGCTGGCCACATACACTGTGCG 579
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1261 lGlnValThrLeuLeuAspThrValGluLeu...ThrTyrCysValArg 1277
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
580  CCTTCGCACTCCACACAGTGGCTCCAGTGAGAAGCGTGAGCTGGCTC 629
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1277 hrPheAlaLeuTyrAsnAsnGlySerSerGlyLysArgLysValArg 1293
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
630  TTTTCACTTCATGCTGCGCAGACCATGAGTTCTCTGATACCCCAACT 679
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1294 PheGlnPheThrAlaTrpProAspHisGlyValProGluHisProThr 1310
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
680  CATCTGCGCTTCTTACGACGGGTCAAGCCCTGCAACCCCTAGACGCG 729
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1310 oPheLeuAlaPheLeuArgArgValLysThrCysAsnProProAspAla 1327
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
730  GCGCCATGGTGTGCTGCACTGACGCGGGCGTGGCGGACCGGCTCTTC 779
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1327 lypProMetValValHisCysSerAlaGlyValGlyArgThrGlyCys 1343
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
780  ATCTGTGATTGATGCTGATGTGAGCGGATGAAGCAGGAGACCGGTGA 829
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1344 lIleValIleAspAlaMetLeuGluArgIleLysHisGluLysThrVal 1360
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
830  CATCTATGGCCCGCTGACCTGCATCGCATCGATCAGAGGAAGTACATG 879
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1360 pIleTyrGlyHisValThrLeuMetArgAlaGlnArgAsnTyrMetVal 1377
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::

880  AGACGGAGGACCACTAGTACGTGTTCATCCATGAGCGCTGTGGAGCTGCC 929
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1377 lnThrGluAspGlnTyrIlePheIleHisAspAlaLeuLeuGluAlaVal 1393
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
930  AGCTGGCGGCACACAGAGTGTCTGCCCGCAACCTGTATGCCACCATCCA 979
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1394 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrAlaTyrIleG 1410
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
980  GAAGCTGGGCCAAGTGCCTCCAGGGGAGAGTGTGACCCCATGGAGCTCG 1029
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1410 nLysLeuThrGlnIleGluThrGlyGluAsnValThrGlyMetGluLeu 1427
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1030  AGTTCAAGTTGTGCTGGCCAGCTCCAGGCCCCACAGCTCCCGCTTCATC 1079
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1427 luPheLysArgLeuAlaSerSerLysAlaHisThrSerArgPheIleSer 1443
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1080  GCCAAGCTGCTCCGCAACCAAGTTCAAGAACCCGCTGCTGAACATCATGC 1129
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1444 AlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetPr 1460
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1130  CTACGAATTGACCCGTGTGTCTGTCAGCCCATCCGTGTGTGGAGGGCT 1179
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1460 oTyrGluSerGlyArgValCysLeuGlnProIleArgGlyValGluGly 1477
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1180  CTGACTACATCAATGCCAGCTTCTCGATGGTTATAGACAGACAGAGGCC 1229
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1477 eAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAla 1493
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1230  TACATAGCTACACAGGGGCTCTGCGAGACCCGAGGACTTCTGGCG 1279
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1494 TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpAr 1510
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1280  CATGCTATGGGAGCACAAATCCACCATCATGCTCATGCTGACCAAGCTTC 1329
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1510 gMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLysLeuAla 1527
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1330  GGAGATGGCGAGGAGAAATGCCACAGTACTTGGCCAGCAGAGCGCTCT 1379
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1527 rGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSer 1543
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1380  GCTCGTACCACTACTTTGTTGTTGATCCCGATGGCTGAGTACAACATGCC 1429
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1544 AlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPr 1560
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1430  CCAGTATATCTCTGCTGCTGAGTTCAAGTCAAGTCAGGATCCCGGATGG 1479
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1560 oGlnTyrIleLeuArgGluPheLysValThrAspAlaArgAsp...GlnS 1576
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1480  CAAGGACAAATCCGGCAGTTCACAGTTCACAGCTGGCCAGAGAGCGCTG 1529
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1576 eArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1592
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1530  CCCAAGACAGCGGAGGATTCATTGACTTTCATCGGCGCAGGTGCATAAG 1579
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1593 ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysTh 1609
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1580  CAAGGACAGCTTTGGACAGATGGGCTTATCAGGTGCTGCTGCTGCTGCTG 1629
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1609 rLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerAlaG 1626
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1630  GGTGGGCGCCAGCGGGGTGTTCACTACTCTGAGCATCTGCTGGAGCGC 1679
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1626 lYvalGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArg 1642
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1680  ATCGCTATGAGGGGTGTGTCGACATGTTTTCAGACCGTGAAGACCCCTGC 1729
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1643 MetArgTyrGluGlyValValAspIlePheGlnThrValLysMetLeuAr 1659
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1730  TACACAGCGTCTGCCATGGTGCACAGAGGACCATGATCATGCTGCTGCT 1779
|||  ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1659 gThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCysT 1676
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1780 ACCCTGCGCCCTGGAGTACCTCGGCAGCTTTGACCACCTATGCAACG 1826
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1676 yrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1691

seq_name: pir2:C54689

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursors

N:Alternate names: MPTP delta type B/C

N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C:Species: Mus musculus (house mouse)

C:Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999

C:Accession: C54689; B54689

R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H. Mol. Cell. Biol. 13, 5513-5523, 1993

A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized

A:Reference number: A54689; MUID: 93360986

A:Accession: C54689

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1894 <MI2>

A:Experimental source: brain; splice form B

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBI:137486, NCBIP:137487)

A:Accession: B54689

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>

A:Experimental source: brain; splice form C

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBI:136527, NCBIP:136530)

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; og

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:45-107/Domain: immunoglobulin homology <IMM1>

F:245-299/Domain: immunoglobulin homology <IMM2>

F:317-399/Domain: fibronectin type III repeat homology <FN3A>

F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1542/Binding site: substrate phosphate (Arg) #status predicted

F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1832/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality:	2874.50	Length:	599
Ratio:	4.956	Gaps:	3
Percent Similarity:	96.828	Percent Identity:	89.149

alignment_block:

US-09-743-492-1 x C54689

Align seg 1/1 to: C54689 from: 1 to: 1894

[illegible]

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1230 TACATAGCTACACAGGGGCTCTGGCAGAGACACCGAGACTTCTGGCG 1279
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1697 TyrIleAlaThrGlnGlyProLeuAlaGluThrGluAspPheTrpAr 1713
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1280 CATGCTATGGGAGACAAATTCACCATCATCGTCATGTCGACCAAGCTTC 1329
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1713 gMetLeuTrpGluHisAsnSerIleValValMetLeuThrLysLeuA 1730
|||||
1330 GGGAGATGGCCAGGAGAAATGCCACGACTACTGGCCAGCAGCGCTCT 1379
|||||
1730 rgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSer 1746
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1380 GTCGCTACCACTACTTTGTTGACCCGATGGCTGAGTACAACATGCC 1429
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|||||
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|||||
1763 oGlnTyrIleLeuArgGluPheLysValThrAspAlaArgAsp...Glns 1779
|||||
1480 CAAGACAAATCCGGCAGTTCACAGTTCACAGACTGGCCAGACGAGCGCTG 1529
|||||
1779 eArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1795
|||||
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1796 ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysTh 1812
|||||
1580 CAAGGACAGTGTGGACAGGATGGCCCTACCGTGCAGTGCAGTGTGCTG 1629
|||||
1812 rLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerAlaG 1829
|||||
1630 GCGTGGCGCCGCGGGGTTCATCTCCTGAGTCTGCTGCTGAGCGC 1679
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1829 lYValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArg 1845
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1680 ATGCGCTATGAGGGCGTGTGCACATGTTTCAGACCGTGAAGACCCCTGG 1729
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1846 MetArgTyrGlyGlyValValAspIlePheGlnThrValLysMetLeuAr 1862
|||||
1730 TACACAGCTGCTCGCATGGTCCACAGACGAGACCATCATCAGTGTGCT 1779
|||||
1862 gThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCysT 1879
|||||
1780 ACCGTGGCGCCCTGGAGTACCTCGGCGAGCTTTGACCACTATGCAACG 1826
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1879 yrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1894

seq_name: pir2: I50212

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: I50212

R:Stoker, A.W.

Mech. Dev. 46, 201-217, 1994

A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase ar

A:Reference number: I50212; MUID:95001563

A:Accession: I50212

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1499 <STO>

A:Cross-references: GB:L32780; NID:g485746; PIDN:AAA64460.1; PID:g485747

C:Genetics:

A:Gene: CRYPalpal

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
P:148-208/Domain: immunoglobulin homology <IMM1>
F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <3PR>
F:881-1479/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1147/Binding site: substrate phosphate (Arg) #status predicted
F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1438/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2867.50 Length: 599

Ratio: 4.944

Percent Similarity: 96.828 Percent Identity: 87.980

alignment_block:

US-09-743-492-1 x I50212

Align seg 1/1 to: I50212 from: 1 to: 1499

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80 TATCGAGACACCCACCATCCCATCACCGCTGGCGGACACATCG 129
||| :|||
918 yMetLeuSerHisProIleProValSerGluLeuAlaGluHisThrG 935
||| :|||
130 ACGGCTCAAGCCCAACGATGGCTCAAGTCTCCAGGAGTATGAGTCC 179
||| :|||
935 luhHisLeuLysAlaAsnAspAsnLeuLysLeuSerGlnGluTyrGluSer 951
||| :|||
180 ATGACCCCTGGACAGCTTCACGTGGGAGAAATCAACCTCGAGGTGAA 229
||| :|||
952 IleAspProGlyGlnGlnPheThrTyrGluHisSerAsnLeuGluValAs 968
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230 CAAGCCCGAGAACCGCTATGCGAATGTCATCGCTACGACCACTCTCGAG 279
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968 nLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgv 985
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1002 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGln 1018
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380 CCCCCTGGCCGAGACCATGGCGGATTTCTGGAGAAATGGTGTGGGAACAGC 429
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1018 yProLeuProGluThrPheGlyAspPheTrpArgMetValTrpGluGlnA 1035
||| :|||
430 GCACGGCCACTGTGTCATGATGACACGCTGGAGGAGAGTCCCGGTA 479
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530 TCAGTGACCCCTGTGGACACATGGAGCTGGCCACATACACTGTGCCGA 579
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630 TTTCAGTTTCATGGCTGGCCGACCATGGAGTCTCTGAGTACCCCACTCC 679
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1102 PheGlnPheThrAlaTrpProAspHisGlyValProGluTyrProThrPr 1118
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680 CATCCCTGGCTTCCTACGAGGCTCAAGCCCTGCAACCCCTAGACGCAG 729
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730 GGCCCATGTTGCTGCTACTACGAGCGGGCGTGGCGCCACCGCTGCTTC 779
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1135 lyProileValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1151
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780 ATCGTGATTGATGCCATGTTGAGCGGGATGAAGCAGCAGAACGCTGGA 829
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1152 IleValIleAspAlaMetLeuGluArgIleLysHisGluLysThrValAs 1168
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830 CATCTATGCCACGTGACCTGATCGGATGATCAGACAGAGAACTACATGCTC 879
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1168 pIleTyrGlyHisValThrLeuMetArgSerGlnArgAsnTyrMetValG 1185
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880 AGACGAGGACCATGACGTGTTTCATCCATGAGCGCTGCTGGAGGCTGCC 929
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1185 InThrGluAspGlnTyrSerPheIleHisAspAlaLeuLeuGluAlaVal 1201
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930 AGTGGCGGCACACAGAGTGGCTGCCGCCACCTGTATGCCACATCCA 979
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1202 AlaCysGlyAsnThrGluValProAlaArgAsnLeuTyrThrTyrIleG 1218
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980 GAAGCTGGCGCCAAAGTGCCTCCAGGGGAGAGTGTACCCGCATGGAGCTCG 1029
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1218 nLysLeuAlaGlnIleGluValGlyGluHisValThrGlyMetGluLeuG 1235
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1030 AGTTCAAGTTGCTGGCCACTCCTCAAGGCCACACGTCCTCGCTTCATCAGC 1079
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1080 GCCAAGCTCCCTGCAACAGTTCAGAACCGCTGCTGAACATCATGCC 1129
|||||
1252 AlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetPr 1268
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1130 CTACGAATTCACCCGTGTGTCTGTCAGAGCCCATCGTGTGTGGAGGGCT 1179
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1268 oTyrGluThrThrArgValCysLeuGlnProIleArgGlyValGluGlyS 1285
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1330 GGGAGATGGCAGGAGAAATGCCACCATCTGCTGCGCAGCAGAGCGCTCT 1379
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1380 GTCGCTACCACTACTTGTCTGACCGGATGGCTGAGTACAAATGCC 1429
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1352 AlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPr 1368
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1430 CCAGTATATCCCTGCTGAGTTCAGAGTCCAGGATGCCGGATGGGCAGT 1479
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1368 oGlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnS 1385
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1480 CAAGACAAATCCGGGATTCAGTTCAGATTCACAGACTGCCAGAGAGCGGTG 1529
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1385 eArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnGlyVal 1401
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1530 CCAAGACAGCGGAGGATTCATGCTTCATCCTGCGGCGAGGTGCATAAGAC 1579
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1780 ACCGTGCGGCCCTGGAGTACCTCGCGAGCTTTGACCACTATGCAAGC 1826
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seq_name: pir2:I58148
seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: I58148; S46218
R:Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993
A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neuro
A:Reference number: I58148; MUID:93357030
A:Accession: I58148
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1501 <WAL>
A:Cross-references: GB:L19933; NID:g310242; PIDN:AAA42309.1; PID:g310243
A:Note: In Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattu
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-
A:Reference number: S46218; MUID:94347119
A:Accession: S46218
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-1501 <ZHA>
A:Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
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C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyr
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F:246-300/Domain: immunoglobulin homology <IMM3>
F:413-506/Domain: fibronectin type III repeat homology <3FR>
F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <PTP1>
F:969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
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F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
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F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted
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Percent Similarity: 96.828 Percent Identity: 87.312
alignment_block:
US-09-743-492-1 x I58148
Align seg 1/1 to: I58148 from: 1 to: 1501
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seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S50893; S40281
R:Wagner, J.; Boerboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994
A:Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
A:Reference number: S50893; MUID:95112841
A:Accession: S50893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1907 <WAG>
A:Cross-references: EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g587484
R:Handriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
Submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases
A:Reference number: S40280
A:Accession: S40281
A:Molecule type: mRNA
A:Residues: 1441-1501, 'E', 1503-1546 <HEN>
A:Cross-references: EMBL:Z23050; NID:g438137; PIDN:CAA80585.1; PID:g438138
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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F:246-300/Domain: immunoglobulin homology <IMM2>
F:413-506/Domain: fibronectin type III repeat homology <3FR>
F:1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
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F:1554/Binding site: substrate phosphate (Arg) #status predicted
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1442	rgSerAlaThrValValMetMetThrArgLeuGluGlySerArgIle	1458
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1625	nLysLeuAlaGlnValGluProGlyGluHisValThrGlyMetGluLeuG	1642
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1692	erAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnLysAla	1708
1230	TATACATAGCTACAGGGCGCTCTGGCAGAGACACCGAGACTTCGGCG	1279
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seq_name: pir2:S46217

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
Alternate names: leukocyte common antigen-related phosphatase

Species: Rattus norvegicus (Norway rat)

C>Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C/Accession: S46217; S51174; A49104

Biochem. J. 302, 39-47, 1994

A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph

A/Reference number: S46216; MUID:94347119

A/Accession: S46217

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1863 <ZHA>

A/Cross-references: EMBL:L11587

R/Goldstein, B.J.

submitted to the EMBL Data Library, February 1993

A/Reference number: S51174

A/Accession: S51174

A/Molecule type: mRNA

A/Residues: 1-1788, 'G', 1790-1863 <GOI>

A/Cross-references: EMBL:L11587; NID:g205134; PID:AAC37656.1; PID:g205135

R/Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silven

J. Biol. Chem. 268, 24880-24886, 1993

A>Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ner

A/Reference number: A49104; MUID:94043351

A/Accession: A49104
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
A/Experimental source: brain
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C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
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C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
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F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-592/Domain: fibronectin type III repeat homology <FN3C>
F;1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
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F;1504/Active site: Cys (phosphocysteine intermediate) #status predicted
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Ratio: 4.903 Gaps: 0

Percent Similarity: 96.828 Percent Identity: 87.145

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US-09-743-492-1 x S46217

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seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A48758
 R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
 J. Biol. Chem. 268, 19284-19291, 1993
 A:Title: Cloning and expression of two structurally distinct receptor-linked protein-
 A:Reference number: A48758; MUID:93374907
 A:Accession: A48758
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1496 <PAN>
 A:Cross-references: GB:L19180
 A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as
 as Phe
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
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 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tra
 F:149-209/Domain: immunoglobulin homology <IMM1>
 F:246-300/Domain: immunoglobulin homology <IMM2>
 F:318-405/Domain: fibronectin type III repeat homology <FN3A>
 F:411-504/Domain: fibronectin type III repeat homology <FN3B>
 F:509-599/Domain: fibronectin type III repeat homology <FN3C>
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280 TCATCGTTACCTCTAFCATGGTGCTCCCGGGAGTGACTACATCAATGCC 329
AlIleLeuGlnProLeuGluGlyIleMetGlySerAspTyrlleAsnAla 1000

330 AACTACATCGATGGCTACCGAAGCAGAAATGCCCTACATCGCCACGACGG 379
AsnTyrvAlaspGlytyrArgGlnAsnAlatyrlleAlathrGlnGI 1017

380 CCCCTGCCGACCATGGCGGATTTCTGGGAATGGTGTGGGAACAGC 429
yProLeuProGluThrPheGlyAspPheTrpArgMetValTrpGluGlnA 1034

430 GCACGGCCACTGTGTCTATGATGACACGGCTGGAGGAGAAGTCCCGGTA 479
rGserAlathrValValMetMetThrArgLeuGluGluLysSerArgVal 1050

480 AAATGTGATCAGTACTGGCCACGCCGCTGGCACCGAGACCTGTGGCCCTAT 529
LysCysAspGlnTyTrpProAsnArgglyThrGluThrTyrgLyPheII 1067

530 TCAGTGACCCCTGTGGACACAGTGGAGCTGGCCACATACACTGTGGCCA 579
eGInValThrLeuLeuAsppfrrMetGluLeuAlathrPheCysValArgT 1084

580 CCTTCGCACTCCACAAGAGTGGCTCCAGTGAGAAGCTGAGCTGCGTCAG 629
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630 TTTCAGTTTCATGGCTGGCCACAGACCATGGAGTTCCTGAGTACCACTCC 679
PheGlnPheThrAlaTrpProAspHisglyValProGluTyPrOthrPr 1117

680 CATCTCGCCTTCCTACACGGGTCAAGGCCCTCAAGCCCTCAAGCCCTAGACCCAG 729
oPheLeuAlaPheLeuArgArgValLysThrCysAsnProProAspAlag 1134

730 GGCCCATGGTGTGCATCTGCAGCGGGCGGTGGCGCCGACCGGCTGCCTC 779
lyProValValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1150

780 ATCTGTGATTGATGCCATGTTGGAGCGGATGAAGCACGAGAACGGTGGGA 829
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830 CATCTATGGCCACGTGACCTGCATCGCATCACAGAGAACTACATGCTGC 879
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880 AGACGGGAGGACAGTACGTGTTCATTCATGAGGCGCTGCTGGAGGCTGCC 929

1184 InThrGluAspGlnTyrSerPheIleHisGluAlaLeuLeuGluAlaVal 1200
930 ACCTGGCGGCACACAGAGTGCTGCCCGCAACTCTGATGCCACATCCA 979
1201 GlyCysGlyAsnThrGluValProIaIaArgSerLeuTyrThrTyrIleG1 1217
980 GAAGCTGGGCCAAGTGCCCTCCAGGGAGAGTGTGACCGCCATGGAGTCG 1029
1217 nlysLeuAlaGlnValGluProGlyGluHisValThrGlyMetGluLeuG 1234
1030 AGTTCAAGTTGCTGCCAGCTCCAGGCCACACAGTCCCGC...TTTCATC 1076
1234 LuPheLysArgLeuAlaLaProArg...HisThrLeuArgAspSerPhe 1249
1077 AGCGCCAACTCCCTCGCAACAAGTTCAGAACCGGTGTGTGAACATCAT 1126
1250 ThrAlaSerLeuProCysAsnLysPheLysAsnArgLeuValAsnIleLe 1266
1127 GCCTACGAATTTACCCGCTGTGTCTGCACGCCCATCCGGTGGTGGAGG 1176
1266 uProTyrGluSerSerArgValCysLeuGlnProIleArgGlyValGluG 1283
1177 GCCTGACCTACATCAATCCAGCTTCCTGGATGTTATAGACACACAAG 1226
1283 LysSerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLys 1299
1227 GCCTACATAGCTACACAGGGGCTCTGGCAGAGACACCGAGACTTCTG 1276
1300 AlaTyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTr 1316
1277 GCGCATGCTATGGGAGCAAAATCCACCATCATCGTCATGCTGACCAGC 1326
1316 pArgAlaLeuTyrPGLuAsnAsnSerThrIleValValMetLeuThrIysL 1333
1327 TTCGGAGATGGCGAGGAGAAATGCCACCACTACTGCCACAGACAGCGC 1376
1333 euArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArg 1349
1377 TCTGCTCGCTACCACTACTTGTCTTCCACCGCATGGCTGAGTACAACAT 1426
1350 SerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMe 1366
1427 GCGCCAGTATATCTCGGTGAGTTCAGGTCAAGGTACCGATGCCGGATGGC 1476
1366 tProGluTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyG 1383
1477 AGTCAAGGACATCCGGCAGTTCCAGTTTCACAGACTGCCACAGACAGGC 1526
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1527 GTGCCCAACAGACGGCGAGGATTCATTGCATTCATCGGACAGGTGCATAA 1576
1398 AlaProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLys 1414
1577 GACCAAGGACAGTGTGGACAGGATGGCCCTATCACGGTGCACGTGCAGTG 1526
1414 sThrLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerA 1431
1627 CTGGCGTGGCGGCACCGGGGTGTTTCATCTCATCTGAGCATCGTCTCTGG 1676
1431 laGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlu 1447
1677 CGCATCGCTATAGGGCGTGGTGCACATGTTTCAGACCGCTGAAGACCT 1726
1448 ArgMetArgTyrGluGlyValValAspIlePheGlnThrValLysValle 1464
1727 GCGTACACAGCGTCTGCGCATGGTGCACAGAGGACCAAGTATCAGCTGT 1776
1464 uArgThrGlnArgProAlaMetValGlnThrGluAspGluTyrGlnPheC 1481
1777 GCTACCGTGGCGCCCTGGAGTACCTCGCGAGCTTTGACCACTATGCAACG 1826

1481 ysPheGlnAlaLeuGlu...LeuGlySerPheAspHisTyrAlaThr 1496

seq_name: pir2:S53089

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)

N:Alternate names: leukocyte antigen-related protein

C:Species: Anopheles gambiae (African malaria mosquito)

C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S53089

R:Spiders: S.

submitted to the EMBL Data Library, March 1995

A:Description: AnLAR-a transmembrane, receptor-like protein tyrosine phosphatase from the

A:Reference number: S53089

A:Accession: S53089

A:Molecule type: DNA

A:Residues: 1-1231 <SPI>

A:Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550

C:Genetics:

A:Introns: 1026/3; 1070/3; 1209/3

A:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F:208-293/Domain: fibronectin type III repeat homology <3FR>

F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>

F:872/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1163/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1169/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2509.00 Length: 597

Ratio: 4.562 Gaps: 0

Percent Similarity: 92.127 Percent Identity: 75.042

alignment_block:

US-09-743-492-1 x S53089 ..

Align seg 1/1 to: S53089 from: 1 to: 1231

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36  TCTGACCCCTGTGGAGATGGGGAGGCTCACTACCAGACCCAGGTATGCG 85
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635 ThrAspProValAspMetArgIleAsnPheGlnThrProGlyMetI1 651
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
86  AGACCAACCACCATCCCATCACCACCTGGCGGACACATCGAGCGCC 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
651 eSerHisProProlIleSerIleAlaGluLeuProAsnHisValGluProl 668
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 TCAACCCCAACGATGGCCCTCAAGTTCTCCAGGAGTATGAGTCCATCGAC 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
668 euLysAlaAsnAspAsnLeuLysPheSerGlnGluTyrGluSerIleGlu 684
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
186 CTGGGACAGCAGTTACGTGGGAGAAATCAACCTGGAGGTGAACAAGCC 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
685 ProGlyGlnGlnPheThrTrpAspHisSerAsnMetGluValAsnLysPr 701
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 CAAGAACCCCTATGCAATGTCATCGCTACGACCACTCTCGAGTCACTCC 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
701 oLysAsnArgTyrAlaAsnValThrSerTyrAspHisSerArgValIleL 718
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286 TTACCTCTATCATGGCGTCCCGGGAGTGACTACATCAATGCCAACTAC 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
718 euProProlIleGluArgValProGlySerAspTyrIleAsnAlaAsnTyr 734
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336 ATCCGATGCTACCGCAAGCAGAAATGCTACATCGCCACGAGGCCCTT 385
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735 CysAspGlyTyrArgLysHisAsnAlaTyrAlaAlaThrGlnGlyProLe 751
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
386 GCCCGAGACCATGGGGATTTCTGGAGAAATGTTGGGAACACGCGCACG 435
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751 uGlnGluThrPheGlyAspPheTrpArgMetCysTrpGluLeuLysSers 768
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1068 eGLYArgGluLysCysPheGlnTyrTrpProHisGluArgSerValArg 1084
1386 TACCAGTACTTTGTTGTTGACCCGATGGCTGAGTCAACATCCCCAGTA 1435
1085 TyrGlnCysTyrValValAspProIleAlaGluTyrAsnMetProGlnTyr 1101
1436 TATCTCGCTGAGTTCAGGTCAAGTCACGGATCCCGGGATGGCAGTCAAGA 1485
1101 rLysLeuArgGluPheLysValThrAspAlaArgspGlySerArgT 1118
1486 CAATCCGGCAGTTCAGTTCACAGACTGCCAGAGCAGCGCTGCCAAG 1535
1118 hrValArgGlnPheGlnPheIleThrTrpProGluGlnGlyValProLys 1134
1536 ACAGCGGAGGATTCATTGACTTCATCGGGCAGGTGCATTAAGCAAGA 1585
1135 SerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysG 1151
1586 GCAGTTTGGACAGGATGGCCCTTATCACGGTGCAGTGCAGTGGCGTGG 1635
1151 uGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValG 1168
1636 GCCGACCCGGGTGTTCATCACTCTGAGCATGCTCTGGAGCGCATGCGC 1685
1168 LyrGThrGlyValPheIleThrLeuSerIleValLeuGluArgMetGln 1184
1686 TATGAGGGGTGGTGCACATGTTTCAGACCGTGAAGACCTCGGTACACA 1735
1185 TyrGluGlyValLeuAspValPheGlnThrValArgIleLeuArgSerG 1201
1736 GGTCTGCTGCATGGTGCACAGAGAGCAGTATCAGCTGCTGCTACCGTG 1785
1201 nArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCysTyrArg 1218
1786 CGGCCCTGGAGTACCTCGGCAGCTTTGACCACCTATGCAACG 1826
1218 laAlaLeuGluTyrLeuGlySerLeuAspHisTyrAlaThr 1231

seq_name: piri:TDFFLK

seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48) D1AR precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: leukocyte antigen-related protein
C:Species: Drosophila melanogaster
C:Date: 14-Dec-1990 #sequence_revision 02-May-1994 #text_change 22-Jun-1999
C:Accession: A36182
R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989
Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila
Reference number: A36182; MUID:90046860

A:Accession: A36182
A:Molecule type: mRNA
A:Residues: 1-2029 <STR>
A:Cross-references: GB:M27700; NID:g157811; PIDN:AAA28668.1; PID:g157812
C:Genetics:
A:Gene: FlyBase: Lar
A:Cross-references: FlyBase:FBgn0000464
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-2029/Product: leukocyte antigen-related protein #status predicted <MAT>
F:33-1377/Domain: extracellular #status predicted <EXT>
F:50-113/Domain: immunoglobulin homology <IMM1>
F:154-211/Domain: immunoglobulin homology <IMM2>
F:249-303/Domain: immunoglobulin homology <IMM3>
F:321-401/Domain: fibronectin type III repeat homology <FN3A>
F:416-502/Domain: fibronectin type III repeat homology <FN3B>
F:514-599/Domain: fibronectin type III repeat homology <FN3C>
F:610-699/Domain: fibronectin type III repeat homology <FN3D>
F:708-802/Domain: fibronectin type III repeat homology <FN3E>
F:811-896/Domain: fibronectin type III repeat homology <FN3F>

F:909-993/Domain: fibronectin type III repeat homology <FN3G>
F:1006-1091/Domain: fibronectin type III repeat homology <FN3H>
F:1101-1198/Domain: fibronectin type III repeat homology <FN3I>
F:1378-1402/Domain: transmembrane #status predicted <TM>
F:1403-2029/Domain: intracellular #status predicted <INT>
F:1417-2029/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1497-1718/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:51-111,161-209,256-301/Dissulfide bonds: #status predicted
F:176/Binding site: carboxylate (Asn) (covalent) #status predicted
F:1670/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1676/Binding site: substrate phosphate (Arg) #status predicted
F:1961/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1967/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:
Quality: 2503.00 Length: 595
Ratio: 4.576 Gaps: 0
Percent Similarity: 91.933 Percent Identity: 75.126
alignment_block:
US-09-743-492-1 x TDFFLK ..
Align seg 1/1 to: TDFFLK from: 1 to: 2029

36 TCTGACCCCTGTGGAGATGGGAGGCTCACTACCAGACCCAGGTATGCG 85
1433 SerAspProValAspMetArgArgLeuAsnPheGlnThrProGlyMetI 1449
86 AGACACCCACCCATCCCATCCAGCCATCCGCGGACAAACATCGAGCGC 135
1449 eSerHisProProlleProIleSerGluPheAlaAsnHisIleGluArgL 1466
136 TCAAGCCCAACGATGCGCTCAAGTCTCCAGAGTATGAGTCCATCGAC 185
1466 euLysSerAsnAspAsnGlnLysPheSerGlnGluTyrGluSerIleGlu 1482
186 CTGGACACGACGTTCACGTGGGAGATTCAAACCTGGAGGTGAACAAGCC 235
1483 ProGlyGlnGlnPheThrTrpAspAsnSerAsnLeuGluHisAsnLysSe 1499
236 CAAGAACCCGCTATGGGAATGTCTATCGCTCCGCTACGACCATCTCGAGTATCC 285
1499 rLysAsnArgTyrAlaAsnValThrAlaTyrAspHisSerArgValGlnL 1516
286 TTAACCTATCATGATGCGTCCCGGAGTACTACATCAATGCCAATAC 335
1516 euProAlaValGluGlyValValGlySerAspTyrIleAsnAlaAsnTyr 1532
336 ATCGATGGCTACCGAAGCAGATGCTACATCGCCACGCGCCGCGCCCT 385
1533 CysAspGlyTyrArgLysHisAsnAlaTyrValAlaThrGlnGlyProLe 1549
386 GCCCGACGACATGGCGATTTCTGGGAATGTGTGGGAACAGCGCACGG 435
1549 uGlnGluThrPheValAspPheTrpArgMetCysTrpGluLeuLysThrA 1566
436 CCACGTGTGTCTATGATGACACCGCTGGAGGAGAGTCCCGGGTAAATGT 485
1566 laThrIleValMetMetThrArgLeuGluGluArgThrArgIleLysCys 1582
486 GATCAGTACTGCCCGCGCTGGCACCAGACCTGTGGCTTTATTCAGGT 535
1583 AspGlnTyrTrpProThrArgGlyThrGluTyrGlyGlnIlePheVa 1599
536 GACCCCTGTGGACACAGTGGAGCTGGCCACATACACTGTGGCCACCTCG 585
1599 lThrIleThrGluThrGlnGluLeuAlaThrTyrSerIleArgThrPheG 1616
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1616 InLeuCysArgGlnGlyPheAsnAspArgGluIleLysGlnLeuGln 1632

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686 GGCTTCCTACGAGCGGTGAAGCGCTGCAACCCCTAGACGACGAGGCCCA 735
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736 TGCTGTGCTGCTACGCGCGGGCGTGGCGCCACCGCTGCTTCATCGTG 785
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1666 alIleValHisCysSerAlaGlyValGlyArgThrGlyCysTyrIleVal 1682
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836 TGCCACGTCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 885
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886 AGCAGCAGTACGTGTCATCCATGAGCGCTGCTGGAGCGTGGCAGCTGC 935
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1716 LuAspGlnTyrIlePheIleHisAspAlaIleLeuGluAlaIleIleCys 1732
936 GGCCACACAGAGTGGCTGCCGCCAACCTGTATGCCACATCCAGAGCT 985
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1733 GlyValThrGluValProAlaArgAsnLeuHisThrHisLeuGlnLysLe 1749
986 GGCCCAAGTCCCTCCAGGAGAGTGTGACCGCCGCTGAGCTCGATTCGA 1035
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1749 uLeuIleThrGluProGlyGluThrIleSerGlyMetGluValGluPheL 1766
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1336 TGGCAGGAGGAATGCCACGACTACTGGCCACAGAGCGCTGCTGCTGC 1385
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1866 etGlyArgGluLysCysPheGlnTyrTrpProHisGluArgSerValArg 1882
1386 TACCACTACTTTGTTGACCGGATGGCTGAGTACAAATGCCCCAGTA 1435
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1883 TyrGlnTyrTyrValValAspProIleAlaGluTyrAsnMetProGlnTy 1899
1436 TATCTTGGCTGAGTTCAGGTACCGATGCCCGGATGGCGACTCAAGGA 1485
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1899 rLysLeuArgGluPheLysValThrAspAlaArgGlySerSerArgT 1916
1485 CAATCGGCGAGTTCCAGTTCACAGACTGGCCAGACGAGCGGTGCCCAAG 1535
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1916 hrValArgGlnPheGlnPheIleAspTrpProGluGlnGlyValProLys 1932
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1536 ACAGGCGAGGATTTCATTGCTCATGGCAGGTGCATAGACCAAGGA 1585
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1933 SerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGl 1949
1586 GCAGTTTGGACAGATGGGCTATCAGCGTGCAGTGCAGTGCAGTGGCGTGG 1635
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1949 uGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValG 1966
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1686 TATGAGGCGCTGGTGCACATGTTTCAGACCGTGAAGACCGCTGGCTACACA 1735
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1999 nArgProAlaMetValGlnThrGluAspGlnTyrHisPheCysTyrArgA 2016
1786 CGGCCCTGGAGTACCTCGGCAGCTTTTACCACCTAT 1820
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2016 laAlaLeuGluTyrLeuGlySerPheAspAsnTyr 2027

seq_name: pir2:T31093

seq_documentation_block:
probable protein-tyrosine-phosphatase (EC 3.1.3.48) - medicinal leech
N:Alternate names: receptor tyrosine phosphatase
C:Species: Hirudo medicinalis (medicinal leech)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31093
R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997
A:Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cell
A:Reference number: Z20976
A:Accession: T31093
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1437 <GER>
A:Cross-references: EMBL:AF017084; NID:g2695656; PID:g2695657; PIDN:AAB91461.1
C:Gene: LARI
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
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C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra

alignment_scores:
Quality: 2450.50 Length: 608
Ratio: 4.472 Gaps: 3
Percent Similarity: 90.132 Percent Identity: 74.342

alignment_block:
US-09-743-492-1 x T31093 ..
Align seg 1/1 to: T31093 from: 1 to: 1437

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831 LeuSerIleHisProThrAspProVal.....ArgArgLeuGlnTyrGl 845
71 GACCCAGGTATGCGAGACACCCACCCATCCCATCCACGACCTGGCGG 120
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845 nThrGlnAlaMetAlaCysHisProSerIleProIleSerGluPheAla 862
121 ACAACATCGAGCGCTCAAGCCAAAGCCACGATGGCTCAAGTTCCTCCAGGAG 170
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
862 laHisValGluGlnLeuLysAlaCysAsnGlyAlaArgPheSerGlnGlu 878
171 TATGACTTCATCCACCTGGACAGCAGTTCACCTGGGAGAAATTCAAACCT 220
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
879 TyrGluSerIleGluProGlyGlnGlnPheThrTrpGluAlaSerLe 895
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221 GGAGGTGAACAGCCCAAGACCGCTATCGAATGTCATCGCCTAGACC 270
1195 nileuProTyrGluSerArgValThrLeuGlnLeuIleArgGlyV 1212
1171 TGAGGGCTCTGACTACATCAATCCAGCTTCTGATGTTATAGACAG 1220
1212 aAspGlySerAspTyrIleAsnAlaAsnPheIleAspGlyTyrArgTyr 1228
1221 CAGAAGCCCTACATAGTACACAGAGGCGCTCTGGCAGAGACCGAGGA 1270
1229 LysLysAlaTyrIleAlaThrGlnGlyProLeuAlaSerThrThrGluAs 1245
1271 CTCTGCGCATGTATGGAGCACAATCCACCATCATCTGTCATGCTGA 1320
1245 pPheTyrArgMetLeuTyrPheHisAsnSerThrIleValValMetLeuV 1262
1321 CCAAGCTTCGGGAGATGGCAGGAGAAATGCCACGACTACTGGCCAGCA 1370
1262 aLLysLeuArgGluMetGlyArgGluLysCysLeuGlnTyrTrpProSer 1278
1371 GAGCGCTCTGCTGCTACAGTACTTGTGTTGACCCGATGGCTGAGTA 1420
1279 GluArgSerAlaArgTyrGlnTyrPheValValAspPrometValGluTy 1295
1421 CAACATGCCCGCAGTATATCTGCTGAGTTCAGAGTCAAGGTCAAGGATCCCGGG 1470
1295 rAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArgA 1312
1471 ATGGCAGTCAAGGACATCCCGCAGTTCACAGTTCACAGACTGGCCAGAG 1520
1312 spGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTyrProGlu 1328
1521 CAGGCGTGTCCCAAGACAGCGGAGGATTCATGTGACTTTCATCGGGCAGGT 1570
1329 GlnGlyValProLysSerGlyGluGlyPheValAspPheIleGlnVa 1345
1571 GCATAAGACCAAGGACAGTTCGACAGGATGGCGCTATCACGGTGCAC 1620
1345 lHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisC 1362
1621 GCAGTCTGCGTGGCCCGCCAGCGGGTGTTCATCACTCTGACATCGTC 1670
1362 ysGlyAlaGlyValSerArgThrGlyValPheIleAlaLeuSerValVal 1378
1671 CTGGAGCGCATCGCTATGAGGCGGTGGTGGACATGTTTCAGACCGTGAA 1720
1379 LeuGluArgMetArgTyrGluGlyValValAspLeuPheGlnThrValar 1395
1721 GACCCCTGCTACACAGCGTCTGCTGCC.....ATGGTGC 1752
1395 gLeuLeuArgThrGlnArgProCysValLysLeuArgLeuGlnValG 1412
1753 AGACA...GAGGACCATGATCACTGTCTACCGTGGCGCCCTGGAGTAC 1799
1412 lInThrProGluAspHisTyrAlaPheCysTyrArgAlaAlaLeuGluTyr 1428
1800 CTCGGCAGCTTTGACCACTATGCA 1823
1429 LeuGlySerPheArgHisTyrAla 1436
seq_name: pir2:T30938

seq_documentation_block:

receptor tyrosine phosphatase - medicinal leech
C:Species: Hirudo medicinalis (medicinal leech)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C:Accession: T30938

R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.

submitted to the EMBL Data Library, December 1997

A:Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed
A:Reference number: 220939

A:Accession: T30938

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-2051 <GER>
 A:Cross-references: ENBL:AF017083; NID:g2695654; PID:g2695655; PIDN:AAB91460.1
 C:Genetics:
 A:Gene: LAR2
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

alignment_scores:
 Quality: 2377.00 Length: 612
 Ratio: 4.402 Gaps: 2
 Percent Similarity: 88.235 Percent Identity: 71.242

alignment_block:
 US-09-743-492-1 x T30938 ..

Align seg 1/1 to: T30938 from: 1 to: 2051

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39  GACCCCTGTGGAGATGGGGGCTCAACTACGACGCCAGGCTATGGGAGA 88
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1438  AspProValAspValargArgMetGlnPheGlnSerProAlaMetValAs 1454
89  CCACCCACCCATCCCATCCAGCCTGGGGGACACATCGAGCGCTCA 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1454  nHisProProileArgValGluAspLeuAlaThrHisLeuGluAlaLeuA 1471
139  AAGCCCAACGATGCCCTCAAGTCTCCAGGAGTATGAGTCCATCGACCCT 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1471  rGlaSerAspAsnAsnArgPheSerLeuGluTyrGluSerIleAspPro 1487
189  GGACAGCAGTTCACGTGGGAGAATTCAAACCTGGAGGTGAACAGCCAA 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1488  GlyGlnPheThrTrpGluAlaSerAsnLeuGluValAsnLysSerLy 1504
239  GAACCGTATCCGAATGTATCCCTACGACCACTCTCGAGTCACTCTTA 288
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1504  sAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgValThrLeuH 1521
289  CCTCTATC.....GATGGCT 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1521  isProLeuProGlnAlaSerSerThrTyrHisProGlyGlnValVal 1537
306  CCGGGAGTGACTACATCAATGCCAATACATCGATGGCTACCGCAAGCA 355
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1538  ProGlySerAspTyrIleAsnAlaAsnPheLeuAspGlyPheArgLysGI 1554
356  GAATGCTTACATCCGACGAGGCCCCCTGCCCGAGACCATGGCGGATT 405
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1554  nAsnAlaTyrIleAlaThrGlnGlyProMetAlaGluThrSerValAsp 1571
406  TCTGGAGAATGTGTGGGAACAGCGCACCTGTGTGTATGATGACA 455
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1571  heTrpArgMetValTrpGluArgGlnSerProValIleValMetMetThr 1587
456  CGGCTGGAGAGAAGTCCCGGTAAATGTGATCAGTACTGGCCGCCCGCC 505
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1588  LysLeuGluGluArgGlyArgValLysCysAspGlnTyrTrpProSerAr 1604
506  TGGCACCAGACCTGTGGCTTATTAGTGACCCCTGTTGGACACAGTGG 555
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1604  gGlySerGluSerTyrGlySerLeuGlnValAsnLeuValAlaValIleG 1621
556  AGCTGGCCACATACACTGTGGCACCTTCGCACCTCCACAAAGAGTGGCTCC 605
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1621  luLeuAlaThrTyrThrMetArgThrPheGlnMetSerSerGluPheAsn 1637
606  AGTGAGAAGCGTGTAGTGGCTCAGTTTCAGTTTCATGCGCTGGCCAGACCA 655
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1638  SerGluLysArgGluValArgHisPheGlnPheThrAlaTrpProAspTy 1654
656  TGGAGTTCCTGAGTACCACTCCCATCTCGGCTTCCTACGACGGGTCA 705
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```

```

1654  rGlyValProGluHisAlaAlaProLeuLeuLeuPheHisGluGluGlyG 1671
706  AGCCCTGCAACCCCTAGACGCGAGGCCCATGGTGTGCTACTGCAGCGCG 755
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1671  InValHisAspProProAspSerGlyProIleValValHisCysSerAla 1687
756  GCGGTGGCGCGCCGCTCTTCATCGTATGATGATGATGATGATGATGATG 805
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1688  GlyValGlyArgThrGlyValPheValValLeuAspSerMetLeuGluAr 1704
806  GATGAAGACGACGAGACGCGTGCACATCTATGCCACGTCGACCTGCATGC 855
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1704  gIleLysHisThrGlySerValAspIleTyrGlyHisValThrCysLeuA 1721
856  GATCAGACGAGAACTACATGTCGACGAGGAGGACGAGGAGGAGGAGGAG 905
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1721  rGlaGlnArgAsnTyrMetValGlnThrGluAspGlnTyrIlePheIle 1737
906  CATGAGCGCTGCTGGAGGCTGCCAGTCGCGGCACACAGAGGTGCCTGC 955
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1738  HisAlaAlaIleLeuGluAlaValThrSerGlyAsnThrGluValProAl 1754
956  CCGCAACCTGTATGCCACATCCAGAGCTG..... 986
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1754  aArgAsnLeuPheAlaHisMetGlnLysLeuLeuGluProLeuThrIleT 1771
987  .GGCCAAAGTCCCTCCAGGGGAGGTGTGACCGCATGGAGCTCGAGTTC 1034
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1771  hrSerGlnSerGlyHisSerThrThrIleThrGlyIleGluAlaGluPhe 1787
1035  AAGTGTCTGGCCAGCTCCAAAGGCCACACGCTCCGCTTCATCAGCGCAA 1084
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1788  LysLysLeuSerSerGlyLysThrSerLeuSerSerPheAlaSerAlaAs 1804
1085  CTTGCCCTGCACAAGTTCAAGAACCGCGTGTGAGCATCATGCCCTACG 1134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1804  nLeuSerCysAsnLysGlnLysAsnArgLeuValAsnValLeuProTyrG 1821
1135  AATTGACCCGTGTGTCTGCAGCCATCCGTTGGTGTGGAGGCTCTGAC 1184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1821  luThrThrArgValCysLeuGlnProIleArgGlyValAspGlySerAsp 1837
1185  TACATCAATGCCAGCTTCTCGATGTTATAGACGACGAGAAGGCTTACAT 1234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1838  TyrIleAsnAlaSerPheIleAspGlyTyrArgTyrArgAlaTyrIle 1854
1235  AGTACACAGCGGCTCTGCCAGAGCACCAGGAGCTTCTGGCGCATGC 1284
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1854  eAlaThrGlnGlyProLeuProAspThrValGluAspPheTrpArgAlaL 1871
1285  TATGGGACGACAAATTCACCATCATGCTCATGACCAAGCTTCGGGAG 1334
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1871  euTrpGluSerAsnCysAsnIleIleValMetLeuThrLysLeuArgGlu 1887
1335  ATGGGAGGAGAAATGCCACAGTACTTGCCAGCAGAGCGCTCTGCTCG 1384
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1888  MetGlyArgGluMetCysHisGlnTyrTrpProSerGluArgSerAlaAr 1904
1385  CTACCACTACTTGTGTGTTGACCCGATGCTGAGTACCAACATGCCCACT 1434
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1904  gTyrGlnTyrPheValValAspProLeuAlaGluTyrAsnMetProGlnT 1921
1435  ATATCTGCTGCTGAGTTCAAGCTCACGATCCCGGGATGGCAGTCAAGG 1484
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1921  yrIleLeuArgGluPheLysValThrAspAlaArgaspGlyGlnSerArg 1937
1485  ACAATCCGGCAGTTCAGTTCACAGACTGCGCCAGAGAGCGGCTGCCCAA 1534
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1938  ThrMetArgGlnPheGlnLeuThrAspTrpProGluGlnGlyValProse 1954
1535  GACAGCGGAGGATTCATTGACTTCATCGGCGAGGTGCATAAGCAAGG 1584
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1954  rThrGlyAspGlyPheIleAspPheIleGlyGlnThrHisLysThrLysG 1971

```


1585 AGCAGTTTGGACAGGATGGCCCTATCACGGTGCACCTGACGTGCTGGCGTG 1634
|||||
1971 luGlnPheGlyGlnGluGlyProIleAlaValHisCysSerAlaGlyVal 1987
|||||
1635 GGCCGACACGGGGTTCATCACTCTGAGCATCGCTCGCTGGAGCGATGGG 1684
|||||
1988 GlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetAr 2004
|||||
1685 CPTAGAGGCGTGGTGGACATGTTTCAGACCTGAGACCCCTGCGTACAC 1734
|||||
2004 gPheGluGlyAlaValAspValPheGlnThrValAsnValLeuArgThrG 2021
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1735 AGCGTCCCTGCCATGCTGGCAGACAGAGGACCATATCAGCTGTGCTACCGT 1784
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2021 InArgProGlyMetValGlnThrGluGluGlnThrAlaPheCysTyrArg 2037
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1785 GCGGCGCTGAGTACCTGGCAGCTTTGACCACATAT 1820
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2038 AlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 2049

name: pir2: I56540

seq_documentation_block:

C:protein-tyrosine-phosphatase (EC 3.1.3.48) ctp1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: I56540

R:Sahin, M.; Hockfield, S.

J. Neurosci. 13, 4968-4978, 1993

A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.

A:Reference number: I56540; MUID:94045925

A:Accession: I56540

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-398 <RES>

A:Cross-references: EMBL:U03273; NID:g414996; PID:AA52124.1; PID:g414997

C:Genetics:

A:Gene: ctp1

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogg

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <ptp1>

F:225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <ptp>

F:109/Active site: Cys (phosphocysteine intermediate) #status predicted

F:115/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality:	1869.00	Length:	398
Ratio:	4.893	Gaps:	0
Percent Similarity:	95.980	Percent Identity:	87.437

alignment_block:

US-09-743-492-1 x I56540 ..

Align seg 1/1 to: I56540 from: 1 to: 398

423 GAACAGCGACGGCCACTGTGCTCATGTACACGGCTGGAGGAGAGTC 472

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1 GluGlnArgSerAlaThrValValMetThrArgLeuGluGluLysSe 17

473 CCGGGTAAATGTGATCAGTACTGCGCCAGCCGCTGGCCAGACCTGTG 522

|||||

17 rArgValLysCysAspGlnTyrTrpProAsnArgGlyThrGluThrYrG 34

523 GCGTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATACACT 572

|||||

34 lypHeileGlnValThrLeuLeuAspThrMetGluLeuAlaThrPheCys 50

573 GTGCGCACTTCGCACTCCCAAGAGTGCTCCAGTGAGAGCGGTGAGCT 622

|||||

51 ValArgThrPheSerLeuHisLysAsnGlySerSerGluLysArgGluVa 67

623 GGTTCAGTTTTCAGTTTCATGGCTTGGCCACACCATGGAGTTCTCTGAGTACC 672

|||||

67 lArgHisPheGlnPheThrAlaTrpProAspHisGlyValProGluTyrP 84

673 CAACATCCCATCTGCTTCTTACGACGGTCAAGGCCTGCAACCCCTTA 722

|||||

84 roThrProPheLeuAlaPheLeuArgArgValLysThrCysAsnProPro 100

723 GACGAGGCGCCATGGTGTGTGCTGACGTGACGGGGGGTGGCGCGCACCGG 772

|||||

101 AspAlaGlyProValValValHisCysSerAlaGlyValGlyArgThrGl 117

773 CNGCTTCATCGTGATTCATGCTGATGCTGAGCGGATGAGAGCAGAGAGA 822

|||||

117 yCysPheIleValIleGlyAlaMetLeuGluArgIleArgThrGluLysT 134

823 CGGTGGACATCTATGGCCACGTGACCTGCATGCATGCATGCATGCATGCAT 872

|||||

134 hrValAspValTyrGlyHisValThrLeuMetArgSerGlnArgAsnTyr 150

873 ATGTGTCAGACGAGGACCATGACGTGCTTCATCATGAGGCGCTGCTGGA 922

|||||

151 MetValGlnThrGluAspGlnTyrSerPheIleHisGluAlaLeuLeuGl 167

923 GGTGCCACGTGCGGCCACACAGAGGTGCTGCGCCGCAACCTGTATGCC 972

|||||

167 uAlaValGlyCysGlyAsnThrGluValProAlaArgThrLeuTyrThrT 184

973 ACATCCAGAAAGTGGCGCCAAAGTCCCTCCAGGGGAGTGTGACCGGCATG 1022

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184 yrIleGlnLysLeuAlaGlnValGluProGlyGluHisValThrGlyMet 200

1023 GAGTCGAGTTCAAGTGTGCTGCGCAGCTCCAAAGGCCACACGTCGCGCT 1072

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201 GluLeuGluPheLysArgLeuAlaSerLysAlaHisThrSerArgph 217

1073 CATCAGCGCCACCTGCGCTGCAACAAGTCAAGAACCCTGGTGAACA 1122

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217 elleThrAlaSerLeuProCysAsnLysPheLysAsnArgLeuValAsnI 234

1123 TCATGCCCTTACCAATGTGACCCCTGTGTGCTGCAGCCCATCGTGGTGTG 1172

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234 leLeuProTyrGluSerArgValCysLeuGlnProIleArgGlyVal 250

1173 GAGGCTCTGACTACATCAATGCCAGCTTCCTGGATGGTTATAGACAGCA 1222

|||||

251 GluGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGl 267

1223 GAAGGCTACATAGCTACACAGGGGCTCTGGCAGAGACGACCGAGGACT 1272

|||||

267 nLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspP 284

1273 TCTGGCGCATGCTATGGGAGCACAATTCACCATCATGCTCATGCTGACC 1322

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284 heTrpArgAlaLeuCysGluAsnAsnSerThrIleValValMetLeuThr 300

1323 AAGTTCGGGAGATGGCAGGAGAGAAATGCCACCATGCTACTGCCACAGCA 1372

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301 LysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGl 317

1373 GCGCTCTGCTCGCTACCTACTTGTGTTGTTGACCCGATGGCTGAGTACA 1422

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317 uArgSerAlaArgTyrGlnTyrPheValValAspPheMetAlaGluTyrA 334

1423 ACATGCCCGCATATATCTCTGCTGCTGAGTTCAGGTCAAGTCCAGGTACCGGGAT 1472

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334 snMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArgasp 350

1473 GGGCAGTCAAGCAATCGGCGAGTTCAGTTTCAGACTGCCAGAGCA 1522

|||||

351 GlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGl 367

1523 GGCGTGGCCCAAGACAGCGGAGGATTGATTCATGCTTCATCGGCGAGGTGC 1572
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
367 nGlyAlaProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValH 384
1573 ATAGACCAAGGAGCAGTTGGACAGATGGGCTATCAGCGTG 1616
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
384 iSLysThrLysGluGlnPheAlaGlnAspGlyProIleSerVal 398

seq_name: pir2:T19121

seq_documentation_block:

probable protein-tyrosine-phosphatase (EC 3.1.3.48), receptor C09D8.1 - Caenorhabditis e

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T19121; T21940

R:Coles, L.

submitted to the EMBL Data Library, November 1994

A:Reference number: Z19075

A:Accession: T19121

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1585 <WIL>

A:Cross-references: EMBL:Z46811; PIDN:CA86842.1; GSPDB:GN00020; CESP:C09D8.1

A:Experimental source: clone C09D8

R:Swanburne, J.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19490

A:Accession: T21940

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1585 <W12>

A:Cross-references: EMBL:Z49938; PIDN:CAA90189.1; GSPDB:GN00020; CESP:C09D8.1

A:Experimental source: clone F38A3

C:Genetics:

A:Gene: CESP:C09D8.1

A:Map position: 2

A:Introns: 51/1; 67/3; 156/1; 227/1; 274/3; 311/3; 356/1; 459/1; 487/3; 546/3; 718/3; 81

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: phosphoric monoester hydrolase

alignment_scores:

Quality: 1836.50 Length: 578

Ratio: 3.771 Gaps: 1

Percent Similarity: 84.256 Percent Identity: 56.574

alignment_block:

US-09-743-492-1 x T19121 ..

Align seg 1/1 to: T19121 from: 1 to: 1585

90 CACCCACCCATCCCATCCAGCGGAGGATTGATTCATGCTTCATCGGCGAGGTGC 139
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1009 HisProAlaValProIleAlaGluLeuAlaAsnHisIleGluLeuAr 1025

140 AGCCACGATGGCTCAAGTCTCCAGGATGATGATTCATCGGCGAGGTGC 189

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1025 gmetAsnAsnAlaGlyPheGlnSerGluPheGluSerIleGluThrG 1042

190 GACAGAGTTCACGCGGAGGATTCACAACTGGAGGTGAACAGCCCAAG 239

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1042 LysGlnHisPheThrTrpGluHisSerSerAlaAspMetAsnLysHisLys 1058

240 AACCGTATCGGAATGATCGCTACGACCTCTCGAGTCACTTCCTTAC 289

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1059 AsnArgTyrAlaAsnValAlaAlaTyrAspHisSerArgValValLeuSe 1075

290 CTCTATCGATGGCGTCCCGGAGTGCTACATCAATGCAACTACATCG 339

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1075 rAsnValGluGlyTyrProGlyMetAspTyrIleAsnAlaAsnTyrValA 1092

340 ATGCTACCCGCAAGACAGATGCTACATCGCCAGCGGCGCCCTGCCC 389

1092 spcLYtyrAspLysProArgSerTyrIleAlaThrGlnGlyProLeuPro 1108

390 GAGACCATGGCGGATTTCTGGCAANTGGTGGGAACAGCGCAGGCCAC 439

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1109 GluThrPheSerAspPheTrpArgMetValTrpGluGlnSerValTh 1125

440 TGTGGTCATGATCACAGCGCTGGAGGAGAGTCCCGGTAATAATGTGATC 489

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1125 rIleValMetLeuThrAsnLeuGluGluArgSerArgValLysCysAspG 1142

490 AGTACTGGCCAGCCCGTGGCCACCGACCTGTGGCCTTATTTCAGGTGACC 539

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1142 InfytrpProSerArgGlyThrAlaThrTyrGlyAspIleGluValThr 1158

540 CTGTTGGACACAGTGGAGTGGCCACATACACTGTGGCACCTCCGCACT 589

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1159 LeuLeuGluSerValHisLeuAlaHisTyrThrMetArgThrMetArgLe 1175

590 CCACAAGAGTGGCTCCAGTGGAGAGCGGTGAGTCGCTCAGTTTCAGTTCA 639

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1175 uLysMetValGlyGluProGluValArgGluIleLysHisLeuGlnTyrT 1192

640 TGGCTGGCCAGACCATGGAGTTCTGAGTACCCAACTCCCTCCCTGGCC 689

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1192 hrAlaTrpProAspHisGlyValProAspHisProThrProPheLeuIle 1208

690 TTCCTAGCAGCGGTCAAGGCTCAACCCCTAGACGCGGCGCCCATGGT 739

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1209 PheLeuLysArgValLysThrLeuAsnProAsnAlaGlyProIleI 1225

740 GGTGCTACTGAGCGCGGCTGGCGCGCACCGCTGCTTCATCGTGAATG 789

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1225 eSerHisCysSerAlaGlyIleGlyArgThrGlyAlaPheIleValIleA 1242

790 ATGCCATGTTGGACGGATGAACACAGAGAGCGGTGGACATCTATGGC 839

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1242 spcYsMetLeuGluArgLeuArgTyrAspAsnThrValAspIleTyrGly 1258

840 CAGTGCACCTGCATGCATCACAGAGAACTACATGTCGACAGCGGAGGA 889

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1259 CysValThrAlaLeuArgAlaGlnArgSerTyrMetValGlnThrGluG 1275

890 CCAGTACGTGTTTCATCATGAGCGCTGCTGGAGGTGCCACGCTGGCGCC 939

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1275 uGlnTyrIlePheIleHisAspAlaValLeuAspAlaValAsnSerGlyS 1292

940 ACACAGAGTGCCTGCGCGCAACCTGTATGCCACATCCAGAGAGCTGGGC 989

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1292 erThrGluValProAlaSerArgLeuHisGlnHisLeuHisIleLeuSer 1308

990 CAAGTGCCTCCAGGGAGAGTGTGACCGCCATGGAGCTCGAGTTCAGTT 1039

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1309 Gln...ProSerAlaAspGlnLeuSerGlyIleAspMetGluPheArgH 1324

1040 GCTGGCAGCTCCCAAGGCCACACGCTCCCGCTTCATCAGCGCCCAACTGC 1089

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1324 sleuThrThrLeuLysTrpThrSerAsnArgCysThrValAlaAsnLeuP 1341

1090 CTTGCAACAAGTTCAAGAACCGGCTGGTGAACATCATGCCCTACGAATTG 1139

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1341 roValAsnArgProLysAsnArgMetLeuSerAlaValProTyrAspSer 1357

1140 ACCCGTGTGTGTCGACGCCCATCCGCTGGTGTGGAGGGCTCTGACTACAT 1189

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1358 AsnArgValIleMetArgLeuLeuProGlyAlaAspGlySerAspTyrI 1374

1190 CAATGCCAGCTTCTCGATGTTATAGACAGCAGAGAGAGGCTACATAGCTA 1239

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

1374 eAsnAlaSerTrpIleAspGlyTyrLysGluArgGlyAlaTyrIleAlaT 1391

1240 CACAGGGGCTCTGGCAGAGACCGGAGGACTTCTGGCGCATGCTATGG 1289

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